

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.

Application Serial Number: 10/550,363
Source: IFWP
Date Processed by STIC: 1/16/07

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 01/16/2007

PATENT APPLICATION: US/10/550,363

TIME: 14:33:23

Input Set : F:\Sequence Listing PB60024.ST25.txt

Output Set: N:\CRF4\01162007\J550363.raw

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3 <110> APPLICANT: Glaxo Group Limited
5 <120> TITLE OF INVENTION: Anti-MAG Antibodies
7 <130> FILE REFERENCE: PB60024
9 <140> CURRENT APPLICATION NUMBER: 10/550,363
C--> 10 <141> CURRENT FILING DATE: 2005-09-19
12 <160> NUMBER OF SEQ ID NOS: 17
14 <170> SOFTWARE: PatentIn version 3.3
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 17
18 <212> TYPE: PRT
19 <213> ORGANISM: Artificial
21 <220> FEATURE:
22 <223> OTHER INFORMATION: Light chain Complementarity Determining Region according to
Kabat
24 <400> SEQUENCE: 1
26 Lys Ser Ser His Ser Val Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu
27 1 5 10 15
30 Ala
34 <210> SEQ ID NO: 2
35 <211> LENGTH: 7
36 <212> TYPE: PRT
37 <213> ORGANISM: Artificial
39 <220> FEATURE:
40 <223> OTHER INFORMATION: Light chain Complementarity Determining Region according to
Kabat
42 <400> SEQUENCE: 2
44 Trp Ala Ser Thr Arg Glu Ser
45 1 5
48 <210> SEQ ID NO: 3
49 <211> LENGTH: 8
50 <212> TYPE: PRT
51 <213> ORGANISM: Artificial
53 <220> FEATURE:
54 <223> OTHER INFORMATION: Light chain Complementarity Determining Region according to
Kabat
56 <400> SEQUENCE: 3
58 His Gln Tyr Leu Ser Ser Leu Thr
59 1 5
62 <210> SEQ ID NO: 4
63 <211> LENGTH: 5
64 <212> TYPE: PRT
65 <213> ORGANISM: Artificial
67 <220> FEATURE:
68 <223> OTHER INFORMATION: Heavy chain Complementarity Determining Region according to

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Kabat

70 <400> SEQUENCE: 4

72 Asn Tyr Gly Met Asn

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73 1          5
76 <210> SEQ ID NO: 5
77 <211> LENGTH: 17
78 <212> TYPE: PRT
79 <213> ORGANISM: Artificial
81 <220> FEATURE:
82 <223> OTHER INFORMATION: Heavy chain Complementarity Determining Region according to
Kabat
84 <400> SEQUENCE: 5
86 Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe Thr
87 1          5          10          15
90 Gly
94 <210> SEQ ID NO: 6
95 <211> LENGTH: 17
96 <212> TYPE: PRT
97 <213> ORGANISM: Artificial
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Heavy chain Complementarity Determining Region according to
Kabat
102 <400> SEQUENCE: 6
104 Asn Pro Ile Asn Tyr Tyr Gly Ile Asn Tyr Glu Gly Tyr Val Met Asp
105 1          5          10          15
108 Tyr
112 <210> SEQ ID NO: 7
113 <211> LENGTH: 475
114 <212> TYPE: PRT
115 <213> ORGANISM: Artificial
117 <220> FEATURE:
118 <223> OTHER INFORMATION: Mouse/human chimeric anti-MAG antibody heavy chain
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122 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
123 1          5          10          15
126 Val His Ser Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
127          20          25          30
130 Pro Gly Glu Thr Asn Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
131          35          40          45
134 Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
135          50          55          60
138 Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala
139 65          70          75          80
142 Asp Asp Phe Thr Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
143          85          90          95
146 Thr Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asn Glu Asp Thr Ala Thr
147          100          105          110
150 Tyr Phe Cys Ala Arg Asn Pro Ile Asn Tyr Tyr Gly Ile Asn Tyr Glu
151          115          120          125
154 Gly Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
155          130          135          140
158 Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
159 145          150          155          160
162 Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp

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163                               165                               170                               175
166 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
167                               180                               185                               190
170 Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
171                               195                               200                               205
174 Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
175                               210                               215                               220
178 Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
179 225                               230                               235                               240
182 Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
183                               245                               250                               255
186 Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu Phe Pro
187                               260                               265                               270
190 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
191                               275                               280                               285
194 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
195                               290                               295                               300
198 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
199 305                               310                               315                               320
202 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
203                               325                               330                               335
206 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
207                               340                               345                               350
210 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
211                               355                               360                               365
214 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
215                               370                               375                               380
218 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
219 385                               390                               395                               400
222 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
223                               405                               410                               415
226 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
227                               420                               425                               430
230 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
231                               435                               440                               445
234 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
235                               450                               455                               460
238 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
239 465                               470                               475
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243 <211> LENGTH: 238
244 <212> TYPE: PRT
245 <213> ORGANISM: Artificial
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Mouse/human chimeric anti-MAG antibody light chain
250 <400> SEQUENCE: 8
252 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
253 1                               5                               10                               15
256 Val His Ser Asn Ile Met Met Thr Gln Ser Pro Ser Ser Leu Ala Val

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257          20          25          30
260 Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser Ser His Ser Val
261          35          40          45
264 Leu Tyr Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
265          50          55          60
268 Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Glu
269 65          70          75          80
272 Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe
273          85          90          95
276 Thr Leu Thr Ile Ile Asn Val His Thr Glu Asp Leu Ala Val Tyr Tyr
277          100          105          110
280 Cys His Gln Tyr Leu Ser Ser Leu Thr Phe Gly Thr Gly Thr Lys Leu
281          115          120          125
284 Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
285          130          135          140
288 Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
289 145          150          155          160
292 Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
293          165          170          175
296 Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
297          180          185          190
300 Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
301          195          200          205
304 Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
305          210          215          220
308 Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
309 225          230          235
312 <210> SEQ ID NO: 9
313 <211> LENGTH: 475
314 <212> TYPE: PRT
315 <213> ORGANISM: Artificial
317 <220> FEATURE:
318 <223> OTHER INFORMATION: Mouse/human chimeric anti-MAG antibody heavy chain
320 <400> SEQUENCE: 9
322 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
323 1          5          10          15
326 Val His Ser Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys
327          20          25          30
330 Pro Gly Glu Thr Asn Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
331          35          40          45
334 Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu
335          50          55          60
338 Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala
339 65          70          75          80
342 Asp Asp Phe Thr Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser
343          85          90          95
346 Thr Ala Tyr Leu Gln Ile Ser Asn Leu Lys Asn Glu Asp Thr Ala Thr
347          100          105          110
350 Tyr Phe Cys Ala Arg Asn Pro Ile Asn Tyr Tyr Gly Ile Asn Tyr Glu

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351          115          120          125
354 Gly Tyr Val Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
355          130          135          140
358 Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser
359 145          150          155          160
362 Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
363          165          170          175
366 Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr
367          180          185          190
370 Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr
371          195          200          205
374 Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
375          210          215          220
378 Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp
379 225          230          235          240
382 Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro
383          245          250          255
386 Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro
387          260          265          270
390 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
391          275          280          285
394 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn
395          290          295          300
398 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
399 305          310          315          320
402 Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val
403          325          330          335
406 Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
407          340          345          350
410 Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys
411          355          360          365
414 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
415          370          375          380
418 Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
419 385          390          395          400
422 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
423          405          410          415
426 Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe
427          420          425          430
430 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
431          435          440          445
434 Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr
435          450          455          460
438 Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
439 465          470          475
442 <210> SEQ ID NO: 10
443 <211> LENGTH: 126
444 <212> TYPE: PRT
445 <213> ORGANISM: Artificial

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 01/16/2007
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Input Set : F:\Sequence Listing PB60024.ST25.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17

VERIFICATION SUMMARY

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Input Set : F:\Sequence Listing PB60024.ST25.txt

Output Set: N:\CRF4\01162007\J550363.raw

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date